**Evolution Lab**

In this lab you will practice graphing, hypothesis testing, statistical analysis and the mechanisms of evolution you have learned. Be sure to save this lab as it contains instructions for performing certain tasks needed for future labs.

**Part 1**

The warbler finch eats seeds for the main part of its diet. A scientist wanted to research how the seed characteristics influenced the finch’s evolution. Finches with thicker beaks are more able to crack open harder seeds than those with thinner beaks. High precipitation tends to make seeds develop softer than areas with low precipitation which produce hard seeds. 2 different samples of finches were captured from 2 population sites, A & B, their beaks were measured, and then they were released back to their appropriate location. The data tables below represent the data collected by the scientist:

Table 1: Population Site A sample data Table 2: Population Site A sample data

Set 1 of beak thickness in mm Set 2 of beak thickness in mm

|  |  |  |
| --- | --- | --- |
| 4.99 | 5.10 | 5.21 |
| 4.99 | 5.12 | 5.26 |
| 5.01 | 5.14 | 5.30 |
| 5.06 | 5.18 | 5.36 |
| 5.09 | 5.19 | 5.37 |

|  |  |  |
| --- | --- | --- |
| 3.15 | 5.14 | 5.24 |
| 5.09 | 5.15 | 5.29 |
| 5.11 | 5.23 | 5.31 |
| 5.11 | 5.23 | 5.32 |
| 5.12 | 5.24 | 5.32 |

**SD 0.54 SE 0.14 SD 0.12 SE 0.03**

**Mean 5.16 Mean 5.07**

Table 3: Population Site B sample data Table 4: Population Site B sample data

Set 1 of beak thickness in mm Set 2 of beak thickness in mm

|  |  |  |
| --- | --- | --- |
| 7.24 | 7.25 | 7.29 |
| 7.24 | 7.26 | 7.29 |
| 7.24 | 7.28 | 7.30 |
| 7.25 | 7.28 | 7.31 |
| 7.25 | 7.28 | 7.31 |

|  |  |  |
| --- | --- | --- |
| 7.02 | 7.13 | 7.23 |
| 7.11 | 7.13 | 7.23 |
| 7.11 | 7.13 | 7.24 |
| 7.12 | 7.15 | 7.24 |
| 7.12 | 7.16 | 7.26 |

**SD 0.07 SE 0.02 SD 0.03 SE 0.01**

**Mean 7.27 Mean 7.16**

*Graphing & Error Bars*

1. Calculate the standard error (SE) & mean for each data set above.

2. Plot the two “**Site A**” sample sets’ means and error bars on graph paper by doing the following:

a. Plot a point for the set 1 mean.

b. Draw a vertical line above the mean point that is up the value of the SE; i.e. If the mean is 5.40 and the SE is 0.12, draw a vertical line from the mean point up 0.12 units until at 5.52 (mean + SE)

c. Repeat for a vertical line below the mean, minus the SE; i.e. If the mean is 5.40 and the SE is 0.12, draw a vertical line from the mean point down 0.12 units until at 5.28 (mean - SE).

d. Complete the error bars by putting a horizontal line intersecting the ends of the error bar.

e. Repeat for the set 2 mean.

3. Repeat step 2 for the two “**Site B**” sample sets.

4. Provide titles, axes labels with units and legends if needed.

5. For the site A data sets, decide if they are similar enough to be considered reliable estimates of the true population mean. If the error bars show overlap, it shows the two means are not significantly different and we can assume they are reliable estimates of the true population mean. No overlap means they are significantly different and not reliable estimates of the true mean.

**YES OVERLAP OF ERROR BARS SO BOTH SAMPLES FOR SITE A ARE RELIABLE ESTIMATES OF THE MEAN (NOT SIGNIFICANTLY DIFFERENT).**

6. Repeat step 5 for the site B data. **NO OVERLAP OF ERROR BARS SO SAMPLES FOR SITE B ARE NOT RELIABLE ESTIMATES OF THE MEAN (ARE SIGNIFICANTLY DIFFERENT)**

7. Under each graph explain your reliability decision from steps 5/6.

*Null Hypothesis Testing by the t-test*

A t-test is used to determine if 2 data sets are statistically different from each other. The results of a-test give a number called the **p-value**, which tells us the probability that the data are different by chance alone. Any value greater than .05 is too high and we would conclude our data are similar just by chance, rather than by some scientific explanation. Values less than or equal to .05 are considered valid and mean there is a difference in our data that is significant.

A null hypothesis is stated in various forms but always ascertains that there will not be a significant difference in data. If the data are significantly different based on the t-test, we make a final decision to reject the null hypothesis. If data are not significantly different based on the t-test, we would accept the null hypothesis. Either way the results need a proposed biological explanation to conclude your results.

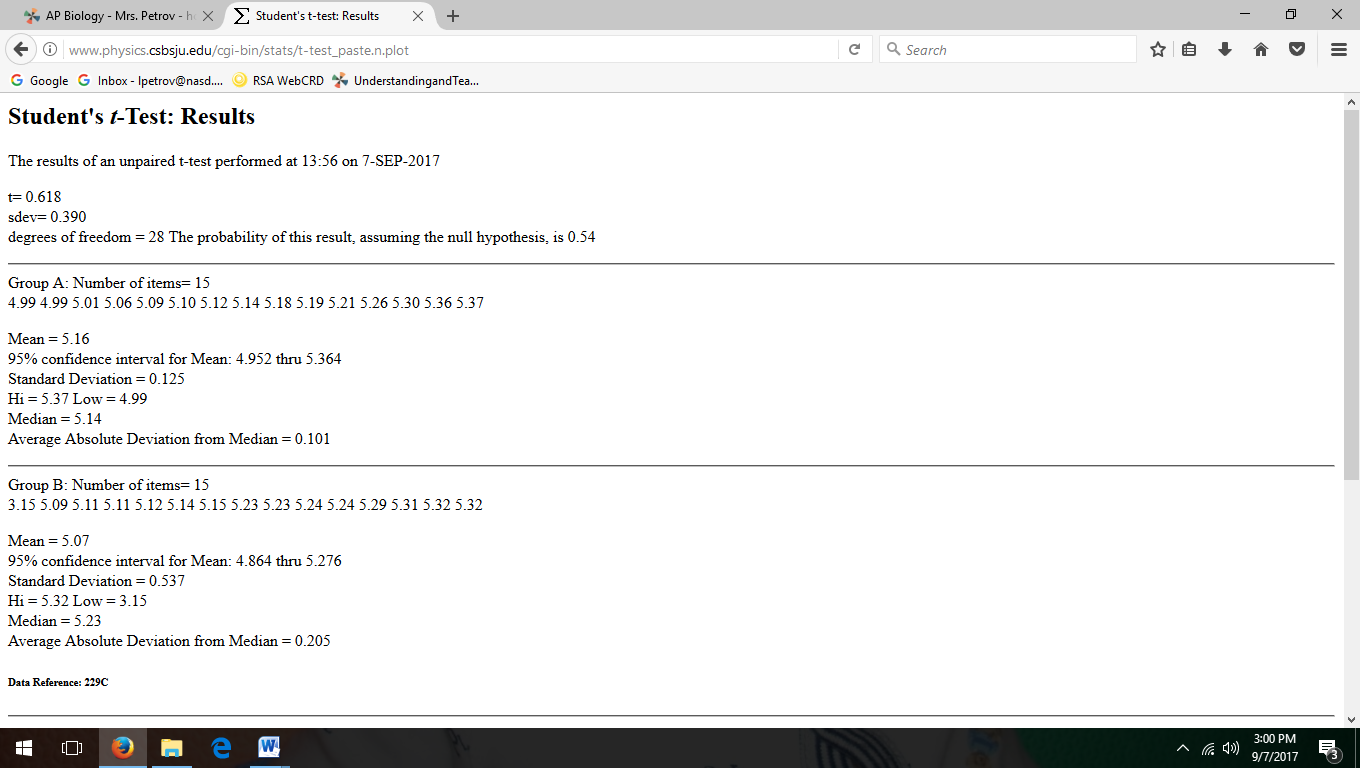
1. Write a null hypothesis concerning the 2 sample sets for population A.

**THERE WILL BE NO SIGINIFICANT DIFFERENCE IN MEAN FINCH BEAK THICKNESS BETWEEN SETS 1 & 2 FROM POPULATION A.**

2. Use the provided website to enter your data and record the p-value below.

http://www.physics.csbsju.edu/stats/t-test\_bulk\_form.html

3. Make a decision about the null hypothesis and explain your results. Keep in mind we are hoping these are statistically similar, meaning there is no difference statistically if p> .05.



**P > 0.05, THEREFORE ACCEPT NULL HYPOTHESIS: MEAN FINCH BEAK THICKNESS IS NOT SIGNIFICANTLY DIFFERENT AMONG SETS 1 & 2 FROM POPULATION A.**

4. Repeat for population B.

**P < 0.05, THEREFORE REJECT NULL HYPOTHESIS: MEAN FINCH BEAK THICKNESS IS SIGNIFICANTLY DIFFERENT AMONG SETS 1 & 2 FROM POPULATION A.**

5. Write a null hypothesis comparing populations A and B. Decide how to pick data for the t-test, **perform the t-test and explain your results. MANY PEOPLE DID NOT DO THIS OR SHOW IT CLEARLY AND POINTS WERE DEDUCTED.**

**Ho: THERE WILL BE NO SIGINIFICANT DIFFERENCE IN MEAN BEAK THICKNESS BETWEEN POPULATIONS A & B.**

**POPULATION A SETS ARE EQUAL IN THEIR RELIABILITY. POPULATION B SETS ARE NOT EQUAL IN THEIR RELIABILITY THOUGH.**

**T-TEST REQUIRES SAME NUMBER OF DATA POINTS IN EACH “BOX”. CHOOSE SETS WITH LOWER STANDARD ERROR TO REDUCE THE RISK OF TOO MUCH STATISTICAL ERROR BIASING THE RESULTS. USE SET 2 FROM POPULATION A & SET 2 FROM POPULATION B.**

**SET 2 DATA FROM POP. A & POP. B SHOULD BE INPUT INTO T-TEST WEBSITE. THE P-VALUE IS LESS THAN .0001 WHICH IS LESS THAN .05 SO THE Ho SHOULD BE REJECTED; DECISION MEANS THAT POP. A & POP. B ARE STATISTICALLY DIFFERENT FROM ONE ANOTHER AND CAN BE CONSIDERED EVOLVING BY NATURAL SELECTION. POP. B LIKELY HAS DRIER CONDITIONS SINCE HARDER DRY SEEDS WILL BE CRACKED AND FED ON BY FINCHES WITH LARGER BEAKS. POP. A LIKELY HAS WETTER CONDITIONS SINCE SOFTER SEEDS CAN BE CRACKED AND EATEN BY THINNER BEAKS.**

**Part 2**

Table 1 – Moth Population “A” over 40 years in Costa Rica

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | 1975 | 1980 | 1985 | 1990 | 1995 | 2000 | 2005 | 2010 | 2015 |
| Population Size | 100,000 | 100,254 | 256 | 268 | 374 | 445 | 613 | 892 | 929 |
| Allele B % | 50% | 53% | 2% | 27% | 52% | 63% | 28% | 35% | 64% |
| Allele b % | 50% | 47% | 98% | 73% | 48% | 37% | 72% | 65% | 36% |

Table 2 – Moth Population “B” over 40 years in Ireland

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | 1975 | 1980 | 1985 | 1990 | 1995 | 2000 | 2005 | 2010 | 2015 |
| Population Size | 100,000 | 100,254 | 100,429 | 100,103 | 100,642 | 101,255 | 101,298 | 102,055 | 102,845 |
| Allele B % | 50% | 53% | 57% | 59% | 67% | 74% | 78% | 83% | 91% |
| Allele b % | 50% | 47% | 43% | 41% | 33% | 26% | 22% | 17% | 9% |

Table 3 – Moth Population “C” over 40 years in USA

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | 1975 | 1980 | 1985 | 1990 | 1995 | 2000 | 2005 | 2010 | 2015 |
| Population Size | 100,000 | 100,254 | 100,429 | 100,103 | 100,642 | 101,255 | 101,298 | 102,055 | 102,845 |
| Allele B % | 10% | 17% | 27% | 42% | 48% | 49% | 50% | 50% | 50% |
| Allele b % | 90% | 83% | 73% | 58% | 52% | 51% | 50% | 50% | 50% |

Table 4 – Moth Population “D” over 40 years in Japan

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | 1975 | 1980 | 1985 | 1990 | 1995 | 2000 | 2005 | 2010 | 2015 |
| Population Size | 100,000 | 100,254 | 100,429 | 100,103 | 100,642 | 101,255 | 101,298 | 102,055 | 102,845 |
| Allele B % | 0% | 0% | 3% | 16% | 28% | 32% | 39% | 25% | 15% |
| Allele b % | 100% | 100% | 97% | 84% | 72% | 68% | 61% | 75% | 85% |

Graph the 4 data sets on separate graph paper. You may put the 4 graphs on 1 paper or on separate papers. The x-axis is each year and the y axis will plot Allele “B” percent in one color and allele “b” in a second color, based on 100%. See example below for formatting. The best way to plot the data is to plot the frequency of one allele like a scatterplot and then shade underneath to represent that allele. Next shade the upper region to the top of the graph in a second color. Be sure each graph has a title to demonstrate which population’s data it represents.



**b**

**B**

*Null Hypothesis Testing by the Chi Square Test*

*The Chi Square Test* – Tests for a statistically significant difference between outcomes of data that we **observe** by an experiment and those we calculate **expected** values for based on a null hypothesis. This test is great for inheritance pattern verifications & category-based data, but it can be used for many other applications also. After performing the Chi Square test, the value known as χ2 (Chi-square) will be the number of interest. If the χ2 value is greater than the critical value in the Chi Square table, we reject the null hypothesis.

1. The null hypothesis that can test if the changes in allele frequencies for the moth population A (table 1) are significant and caused by a specific mechanism is:

*There will be no change in the allele frequencies (dominant or recessive) over the generations.*

Use the null hypothesis & the initial generation year (1975) to discuss what the ***expected*** values should be.

2. Complete the table below to calculate the chi square value.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Categories | Observed values | Expected values | O-E | (O-E)2 | (O-E)2  E |  |
| 1980 |  |  |  |  |  |  |
| 1985 |  |  |  |  |  |  |
| 1990 |  |  |  |  |  |  |
| 1995 |  |  |  |  |  |  |
| 2000 |  |  |  |  |  |  |
| 2005 |  |  |  |  |  |  |
| 2010 |  |  |  |  |  |  |
| 2015 |  |  |  |  |  |  |
|  |  |  |  |  | SUM of ALL = | = χ2 |

3. Critical values are listed in a provided Chi Square Table on your formula sheet. The critical value is always at **the p= 0.05 row** and degrees of freedom is determined by the number of categories minus 1. **Make a decision about the null hypothesis and explain the results in terms of evolution mechanisms.**

**REJECT Ho BECAUSE CHI SQUARE WAS GREATER THAN C.V. THIS MEANS BIOLOGICAL EVOLUTION WAS OCCURING SINCE THE NULL HYPOTHESIS OF ALLELE FREQUENCIES WOULD STAY THE SAME WAS REJECTED.**

Questions: Answer on the pages with your graphs in complete sentences.

1. Which population shows either a mutation occurred or a migration occurred? Explain your answer.

**POP. “D” BECAUSE INITIALLY THERE WAS NO DOMINANT ALLELE IN THE POPULATION BUT APPEARED IN 3RD DATA POINT. ONLY WAY FOR A NEW ALLELE TO BE INTRODUCED IS BY MUTATION OR MIGRATION.**

2. Which population shows genetic drift occurring? Explain your answer using 2 pieces of evidence from the data. **POP. “A” BECAUSE POPULATION SIZE DROPPED SIGNIFICANTLY AND THEREAFTER THE ALLELES SHIFTED RANDOMLY.**

3. The color of moths is controlled by the B/b alleles. The 2 alleles are actually incompletely dominant and the heterozygote (Bb) forms a blend of colors in males that are preferred by females over either of the homozygous varieties (BB or bb). This phenomenon is called “Heterozygote Advantage”, where the heterozygote has some mating advantage in the population. Which population is this reflecting and which mechanism of evolution is causing it? **POP. “C” BECAUSE ALLELES EQUAL OUT WHICH MEANS MOST INDIVIDUALS HAVE EACH ALLELE, THUS ARE HETERZYGOUS. PREFERENTIAL MATING/NON-RANDOM MATING WOULD CAUSE THIS BECAUSE FEMALES PREFER THE HETEROZYGOUS PHENOTYPE AND THOSE MALES REPRODUCE MORE, MAKING SUBSEQUENT GENERATIONS HAVING MOSTLY HETEROZYGOUS INDIVIDUALS.**

4. In Ireland (population “B”) the climate can usually fluctuate but over these 40 years it was much colder than average. The “B” allele codes for a black color and the “b” allele codes for a white color. Darker colors absorb more solar energy and thus heat. Use the data and this scenario to explain why the population allele frequencies changed over generations and how it demonstrates natural selection by survival of the fittest. **THE “B” DOMINANT ALLELE CODES FOR A DARKER COLOR WHICH ABSORBS MORE HEAT. IN AN ENVIRONMENT WHICH IS COLD, THIS ALLELE GIVES INDIVIDUALS MORE HEAT & PROBABLY ENERGY HELPING THEM SURVIVE, DEMONSTRATING SURVIVAL OF THE FITTEST. OVER THESE COLD YEARS THE LIGHT ALLELE WOULD DECREASE IN FREQUENCY BECAUSE INDIVIDUALS WITH A LIGHT PHENOTYPE WOULD NOT BE AS WARM/GET HEAT ENERGY TO SURVIVE AS WELL AS THE DARK INDIVIDUALS. THE DARK INDIVIDUALS ARE SELECTED FOR IN THE COLD ENVIRONMENT, DEMONSTRATING NATURAL SELECTION BY SURVIVAL OF THE FITTEST.**